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RAW SEQUENCE LISTING

DATE: 07/02/2002

PATENT APPLICATION: US/10/076,691

TIME: 13:59:28

Input Set : N:\Crf3\RULE60\10076691.raw

Output Set: N:\CRF3\07022002\J076691.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: SHEPARD, H. M.

6 KAN, NANCY

8 (ii) TITLE OF INVENTION: GENE THERAPY BY RETROVIRAL VECTOR WITH

9 TUMOR SUPPRESSIVE GENE

11 (iii) NUMBER OF SEQUENCES: 2

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP

15 (B) STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

16 (C) CITY: SAN FRANCISCO

17 (D) STATE: CA

18 (E) COUNTRY: U.S.A.

19 (F) ZIP: 94111-3834

ENTERED

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/10/076,691

C--> 29 (B) FILING DATE: 14-Feb-2002

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: US/08/403,797

34 (B) FILING DATE: 04-DEC-1995

36 (A) APPLICATION NUMBER: PCT/US95/08844

37 (B) FILING DATE: 17-SEP-1993

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: FITTS, RENEE A

41 (B) REGISTRATION NUMBER: 35,136

42 (C) REFERENCE/DOCKET NUMBER: 16930-000600

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: (415) 326-2400

46 (B) TELEFAX: (415) 576-0300

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 7 amino acids

53 (B) TYPE: amino acid

54 (C) STRANDEDNESS: Not Relevant

W--> 55 (D) TOPOLOGY: Not Relevant

57 (ii) MOLECULE TYPE: peptide

62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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64      Ser His Arg Pro Gly Ser Arg
65      1          5
67 (2) INFORMATION FOR SEQ ID NO: 2:
69      (i) SEQUENCE CHARACTERISTICS:
70          (A) LENGTH: 428 amino acids
71          (B) TYPE: amino acid
72          (C) STRANDEDNESS: Not Relevant
W--> 73          (D) TOPOLOGY: Not Relevant
75      (ii) MOLECULE TYPE: peptide
80      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
82      Leu Leu Gly Ser Gly Asp Thr Leu Arg Ser Gly Trp Glu Arg Ala Phe
83      1          5          10          15
85      His Asp Gly Asp Thr Leu Pro Trp Ile Gly Ser Gln Thr Ala Phe Arg
86      20          25          30
88      Val Thr Ala Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro
89      35          40          45
91      Leu Ser Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn
92      50          55          60
94      Asn Val Leu Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu
95      65          70          75          80
97      Ser Pro Asp Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp
98      85          90          95
100     Glu Ala Pro Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro
101     100          105          110
103     Ala Ala Pro Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu
104     115          120          125
106     Ser Ser Ser Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe
107     130          135          140
109     Arg Leu Gly Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr
110     145          150          155          160
112     Tyr Ser Pro Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys
113     165          170          175
115     Pro Val Gln Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val
116     180          185          190
118     Arg Ala Met Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val
119     195          200          205
121     Arg Arg Cys Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala
122     210          215          220
124     Pro Pro Gln His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr
125     225          230          235          240
127     Leu Asp Asp Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu
128     245          250          255
130     Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met
131     260          265          270
133     Cys Asn Ser Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr
134     275          280          285
136     Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser
137     290          295          300
139     Phe Glu Val Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu

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140	305	310	315	320
142	Glu Glu Asn Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro			
143		325	330	335
145	Gly Ser Thr Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln			
146		340	345	350
148	Pro Lys Lys Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg			
149		355	360	365
151	Gly Arg Glu Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu			
152		370	375	380
154	Leu Lys Asp Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His			
155	385	390	395	400
157	Ser Ser His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys			
158		405	410	415
160	Lys Leu Met Phe Lys Thr Glu Gly Pro Asp Ser Asp			
161		420	425	

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10076691.raw

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:55 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=1
L:73 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=2